



OIPE

ENTERED

RAW SEQUENCE LISTING

DATE: 08/07/2002

PATENT APPLICATION: US/09/993,420A

TIME: 09:54:15

Input Set : A:\01997.201006.SEQLIST.TXT

Output Set: N:\CRF3\08072002\I993420A.raw

4 <110> APPLICANT: Horvitz, H. Robert
 5 Hengartner, Michael
 7 <120> TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
 8 GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL DEATH AND
 9 USES THEREOF
 11 <130> FILE REFERENCE: 01997/201006
 13 <140> CURRENT APPLICATION NUMBER: US 09/993,420A
 C--> 14 <141> CURRENT FILING DATE: 5001-11-09
 16 <150> PRIOR APPLICATION NUMBER: 09/234,186
 17 <151> PRIOR FILING DATE: 1999-01-20
 19 <150> PRIOR APPLICATION NUMBER: 07/898,933
 20 <151> PRIOR FILING DATE: 1992-06-12
 22 <150> PRIOR APPLICATION NUMBER: 07/927,681
 23 <151> PRIOR FILING DATE: 1992-08-10
 25 <150> PRIOR APPLICATION NUMBER: 08/288,295
 26 <151> PRIOR FILING DATE: 1994-08-10
 28 <150> PRIOR APPLICATION NUMBER: 08/801,248
 29 <151> PRIOR FILING DATE: 1997-02-19
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 33 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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 36 <211> LENGTH: 6560
 37 <212> TYPE: DNA
 38 <213> ORGANISM: Caenorhabditis elegans
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 42 <222> LOCATION: (1)...(6559)
 43 <223> OTHER INFORMATION: n = A,T,C or G
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 48 taatttaaaa aaatcaattt cgaattgaaa ttcaactcct actcgttttg aaaatgccaa 180
 49 tcttttaagt aaacttctgg atcgccatt tcttcagaa attccttcaa agtagtggtt 240
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 53 aggataaaag gctcattttt gaagccgaat ttactaaaa tctctagcca tggagtcgat 480
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 57 acttctcgtg ccctgtgcgt gcatttccgc aacaaaattc aacacttgtt ttgaaacgca 720
 58 ccgccctgtt tcttttttca attttgataa gaaaatcagc attgtttcag gatgattaac 780
 59 attccaactg cgattctgtg ccgcttgggc gccagatcgt cgatttccgc ctcctttgga 840

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62 tattcacagt ccgaggcaaa gacgccaatc cagaagttcg gatgggaata cctggtgaag 1020
63 cagcgctcca agaatcgccc aatcgctcca catctcaccg tctaccagcc acaattgacc 1080
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157 <210> SEQ ID NO: 2
158 <211> LENGTH: 1315

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169      1          5          10
171 tat cgg cga cga acg atg gcg act ggc gag atg aag gag ttt ctg ggg      96
172 Tyr Arg Arg Arg Thr Met Ala Thr Gly Glu Met Lys Glu Phe Leu Gly
173 15          20          25          30
175 ata aaa ggc aca gag ccc acc gat ttt gga atc aat agt gat gct cag      144
176 Ile Lys Gly Thr Glu Pro Thr Asp Phe Gly Ile Asn Ser Asp Ala Gln
177          35          40          45
179 gac ttg cca tca ccg agt agg cag gct tcg acg cga aga atg tcc atc      192
180 Asp Leu Pro Ser Pro Ser Arg Gln Ala Ser Thr Arg Arg Met Ser Ile
181          50          55          60
183 gga gag tca att gat gga aaa atc aat gat tgg gaa gag cca agg ctt      240
184 Gly Glu Ser Ile Asp Gly Lys Ile Asn Asp Trp Glu Glu Pro Arg Leu
185          65          70          75
187 gat atc gag gga ttt gtg gtc gac tat ttc acg cac cga atc cgg caa      288
188 Asp Ile Glu Gly Phe Val Val Asp Tyr Phe Thr His Arg Ile Arg Gln
189          80          85          90
191 aac gga atg gaa tgg ttt gga gca ccg gga ttg ccg tgt gga gtg caa      336
192 Asn Gly Met Glu Trp Phe Gly Ala Pro Gly Leu Pro Cys Gly Val Gln
193 95          100          105          110
195 ccg gag cac gaa atg atg cga gtt atg gga acg ata ttc gag aag aag      384
196 Pro Glu His Glu Met Met Arg Val Met Gly Thr Ile Phe Glu Lys Lys
197          115          120          125
199 cac gcg gaa aat ttt gag acc ttc tgt gag cag ctg ctc gca gtg ccc      432
200 His Ala Glu Asn Phe Glu Thr Phe Cys Glu Gln Leu Leu Ala Val Pro
201          130          135          140
203 aga atc tca ttt tca ctg tat cag gat gtg gtt cgg acg gtt gga aat      480
204 Arg Ile Ser Phe Ser Leu Tyr Gln Asp Val Val Arg Thr Val Gly Asn
205          145          150          155
207 gca cag aca gat caa tgt cca atg tct tat gga cgt ttg ata ggt cta      528
208 Ala Gln Thr Asp Gln Cys Pro Met Ser Tyr Gly Arg Leu Ile Gly Leu
209          160          165          170
211 atc tcg ttc ggc ggt ttc gta gct gca aaa atg atg gaa tcc gtg gaa      576
212 Ile Ser Phe Gly Gly Phe Val Ala Ala Lys Met Met Glu Ser Val Glu
213 175          180          185          190
215 ctg cag gga caa gtg cga aac ctc ttc gtt tac aca tcg ctg ttc atc      624
216 Leu Gln Gly Gln Val Arg Asn Leu Phe Val Tyr Thr Ser Leu Phe Ile
217          195          200          205
219 aaa acg cgg atc cgc aac aac tgg aag gaa cac aat cgg agc tgg gac      672
220 Lys Thr Arg Ile Arg Asn Asn Trp Lys Glu His Asn Arg Ser Trp Asp
221          210          215          220
223 gac ttc atg aca ctc gga aaa caa atg aaa gag gac tac gaa cga gca      720

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228 Glu Ala Glu Lys Val Gly Arg Arg Lys Gln Asn Arg Arg Trp Ser Met
229          240          245          250
231 att ggc gct gga gta aca gct gga gcc att gga atc gtt gga gtc gtc 816
232 Ile Gly Ala Gly Val Thr Ala Gly Ala Ile Gly Ile Val Gly Val Val
233 255          260          265          270
235 gtg tgt ggg cgg atg atg ttc agc ttg aag taacgtattc aatttgtgta 866
236 Val Cys Gly Arg Met Met Phe Ser Leu Lys
237          275          280
239 aataattaat ttatgtacaa ctctttacat ttgaatctca ttttkgctca ctgattctct 926
240 catcctttga actggaagaa gtgggaagc taggccacaa attacggctc tctgtgtcga 986
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249 <211> LENGTH: 280
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253 <400> SEQUENCE: 3
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258 Gly Thr Glu Pro Thr Asp Phe Gly Ile Asn Ser Asp Ala Gln Asp Leu
259          35          40          45
260 Pro Ser Pro Ser Arg Gln Ala Ser Thr Arg Arg Met Ser Ile Gly Glu
261          50          55          60
262 Ser Ile Asp Gly Lys Ile Asn Asp Trp Glu Glu Pro Arg Leu Asp Ile
263 65          70          75          80
264 Glu Gly Phe Val Val Asp Tyr Phe Thr His Arg Ile Arg Gln Asn Gly
265          85          90          95
266 Met Glu Trp Phe Gly Ala Pro Gly Leu Pro Cys Gly Val Gln Pro Glu
267          100          105          110
268 His Glu Met Met Arg Val Met Gly Thr Ile Phe Glu Lys Lys His Ala
269          115          120          125
270 Glu Asn Phe Glu Thr Phe Cys Glu Gln Leu Leu Ala Val Pro Arg Ile
271          130          135          140
272 Ser Phe Ser Leu Tyr Gln Asp Val Val Arg Thr Val Gly Asn Ala Gln
273 145          150          155          160
274 Thr Asp Gln Cys Pro Met Ser Tyr Gly Arg Leu Ile Gly Leu Ile Ser
275          165          170          175
276 Phe Gly Gly Phe Val Ala Ala Lys Met Met Glu Ser Val Glu Leu Gln
277          180          185          190
278 Gly Gln Val Arg Asn Leu Phe Val Tyr Thr Ser Leu Phe Ile Lys Thr

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RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 4956,4958,4959,4996,4997,4998,5000,5183,5184,5185,5191,5192
Seq#:1; N Pos. 5230,5231,6189,6191,6205

VERIFICATION SUMMARY

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L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:128 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:4920
L:129 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:4980
L:132 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:5160
L:133 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:5220
L:149 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:6180